## OIPE JUL 23 2003

## SEQUENCE LISTING

Weinmann, Roberto
Einspahr, Howard M.
Krystek, Stanley R.
Sack, John A.
Salvati, Mark E.
Tokarski, John S.
Attar, Riccardo M.
Wang, Chihuei

- <120> CRYSTALLOGRAPHIC STRUCTURE OF THE ANDROGEN RECEPTOR LIGAND BINDING DOMAIN
- <130> BMS-0010
- <140> 09/687,609
- <141> 2000-10-13
- <150> 60/159,394
- <151> 1999-10-14
- <160> 5
- <170> PatentIn version 3.2
- <210> 1
- <211> 260
- <212> PRT
- <213> Rattus sp.
- <400> 1
- Gly Ser His Met Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu Asn 1 5 10 15
- Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His Asp Asn 20 25 30
- Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu 35 40 45
- Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala Leu Pro 50 55 60
- Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile Gln Tyr 65 70 75 80
- Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr 85 90 95

Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn 105 100 Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met 120 . 115 Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu 135 Phe Leu Cys Met Lys Ala Leu Leu Phe Ser Ile Ile Pro Val Asp 150 155 Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile 165 170 Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser 180 185 Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln 200 195 Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys 210 215 220 Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile 235 Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr 250 Phe His Thr Gln 260 <210> 2 <211> 255 <212> PRT <213> Rattus sp. <400> 2 Gly Gln Asp Ile Gln Leu Ile Pro Pro Leu Ile Asn Leu Leu Met Ser

Ile Glu Pro Asp Val Ile Tyr Ala Gly His Asp Asn Thr Lys Pro Asp

25

20

Thr Ser Ser Ser Leu Leu Thr Ser Leu Asn Gln Leu Gly Glu Arg Gln Leu Leu Ser Val Val Lys Trp Ser Lys Ser Leu Pro Gly Phe Arg Asn Leu His Ile Asp Asp Gln Ile Thr Leu Ile Gln Tyr Ser Trp Met Ser Leu Met Val Phe Gly Leu Gly Trp Arg Ser Tyr Lys His Val Ser Gly Gln Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu Asn Glu Gln Arg Met Lys Glu Ser Ser Phe Tyr Ser Leu Cys Leu Thr Met Trp Gln Ile Pro Gln Glu Phe Val Lys Leu Gln Val Ser Gln Glu Glu Phe Leu Cys Met Lys Val Leu Leu Leu Leu Asn Thr Ile Pro Leu Glu Gly Leu Arg Ser Gln Thr Gln Phe Glu Glu Met Arg Ser Ser Tyr Ile Arg Glu Leu Ile Lys Ala Ile Gly Leu Arg Gln Lys Gly Val Val Ser Ser Ser Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Asn Leu His Asp Leu Val Lys Gln Leu His Leu Tyr Cys Leu Asn Thr Phe Ile Gln Ser Arg Ala Leu Ser Val Glu Phe Pro Glu Met Met Ser Glu Val Ile Ala Ala Gln Leu Pro Lys Ile Leu Ala Gly Met Val Lys Pro Leu Leu Phe His Lys 

```
<210> 3
<211> 36
<212> DNA
<213> Artificial
<220>
<223> Synthetic
<400> 3
catatgattg aaggctatga atgtcaacct atcttt
                                                                      36
<210> 4
<211> 24
<212> DNA
<213> Artificial
<220>
<223> Synthetic
<400> 4
                                                                      24
tcactgtgtg tggaaataga tggg
<210> 5
<211> 4
<212> PRT
<213> Artificial
<220>
<223> Synthetic
<400> 5
Gly Ser His Met
```

- 4 -